

**Supplementary Table. 2: Potential and spatial congruence of the active site residues in serine proteases:** Chymotrypsin and subtilisin are a classical example of convergent evolution where the catalytic Ser-His-Asp triad shows virtually similar geometry in the structurally different proteins. D = Pairwise distance in Å. PD = Pairwise potential difference. See Methods section for units of potential.

PDB	Active site atoms(a,b,c)		ab	ac	bc
1A0J	ASP102OD1,SER195OG,HIS57NE2, chymotrypsin	D	7.8	5.6	3.3
		PD	-144.1	-39.2	104.8
1BIT	ASP102OD1,SER195OG,HIS57NE2, chymotrypsin	D	8.0	5.6	3.3
		PD	-120.5	21.4	142.0
1AF4	ASP32OD1,SER221OG,HIS64NE2, subtilisin	D	7.5	4.7	3.3
		PD	-139.4	45.3	184.7
1BH6	ASP32OD1,SER221OG,HIS64NE2, subtilisin	D	6.6	4.9	2.8
		PD	-90.4	32.0	122.4